

# SEQUENCE LISTING

<110> Crane, Edmund H.  
Crane, Virginia C.

<120> Maize Pathogenesis-Related  
Polynucleotide and Methods of Use

<130> 35718/214291

<150> US 60/195,801

<151> 2000-04-10

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 898

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (63)...(674)

<400> 1

ctcgacgca ctcgacgctc attcactgag ccatttactc agatcaccaa ctccagatct	60
ca atg gcg cac tcg cgc agc cac cac ctc ctc ctg ctc ccc gcg	107
Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala	
1 5 10 15	
ccc atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc	155
Pro Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys	
20 25 30	
gcc gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc	203
Ala Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly	
35 40 45	
gcg ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc	251
Ala Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser	
50 55 60	
aac gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg	299
Asn Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala	
65 70 75	
gcg gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg	347
Ala Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala	
80 85 90 95	
gcc gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc	395
Ala Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe	
100 105 110	

gcg gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc 443  
Ala Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser  
115 120 125

tac cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg 491  
Tyr Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly  
130 135 140

cgg tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc 539  
Arg Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys  
145 150 155

ggc acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc 587  
Gly Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys  
160 165 170 175

gcg cag gcc agc tgc gcc acg ggc gcc acg ctc acg ctc tgc ctg tac 635  
Ala Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr  
180 185 190

aac ccg cac ggc aac gtg cag ggc cag agc ccc tac tag ctagctgagg 684  
Asn Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr \*  
195 200

tcatcaggtc gtagcgacgg agcccaactg ccgccgccgg cggcagcggg gtacgtaggt 744  
tcatcagtct tctctagttc ggtcacggaa aggctgtttt gtgggtgtgat ccggtggtgt 804  
tcttggtggt gttgacaact gctttggttt ggtgtatcag cttttgttgc cgggtaaaaa 864  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 898

<210> 2  
<211> 203  
<212> PRT  
<213> Zea mays

<400> 2  
Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro  
1 5 10 15  
Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala  
20 25 30  
Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala  
35 40 45  
Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn  
50 55 60  
Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala  
65 70 75 80  
Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala  
85 90 95  
Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala  
100 105 110  
Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr  
115 120 125  
Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg  
130 135 140  
Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly  
145 150 155 160  
Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala  
165 170 175

Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr Asn  
 180 185 190  
 Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr  
 195 200

<210> 3  
 <211> 612  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (1)...(612)

<400> 3  
 atg gcg cac tcg cgc agc cac cac cac ctc ctc ctg ctc ccc gcg ccc 48  
 Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro  
 1 5 10 15  
 atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc gcc 96  
 Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala  
 20 25 30  
 gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc gcg 144  
 Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala  
 35 40 45  
 ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc aac 192  
 Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn  
 50 55 60  
 gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg gcg 240  
 Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala  
 65 70 75 80  
 gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg gcc 288  
 Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala  
 85 90 95  
 gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc gcg 336  
 Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala  
 100 105 110  
 gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc tac 384  
 Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr  
 115 120 125  
 cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg cgg 432  
 Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg  
 130 135 140  
 tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc ggc 480  
 Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly  
 145 150 155 160  
 acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc gcg 528  
 Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala

165

170

175

cag gcc agc tgc gcc acg ggc gcc acg ctc acg ctc tgc ctg tac aac 576  
 Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr Asn  
 180 185 190

ccg cac ggc aac gtg cag ggc cag agc ccc tac tag 612  
 Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr \*  
 195 200